

CRF Errors Corrected by the STIC Systems Branch

PCT.

Serial Number: 09/807,499

CRF Processed: _____ Date: _____
 Edited by: _____
 Verified by: _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

PCT

RAW SEQUENCE LISTING

DATE: 05/11/2001

PATENT APPLICATION: US/09/807,499

TIME: 13:34:33

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\05112001\I807499.raw

see p. 5

3 <110> APPLICANT: Rosenmund, Christian
 4 Russo, Sebastian
 6 <120> TITLE OF INVENTION: Non-desensitizing AMPA-Receptors
 8 <130> FILE REFERENCE: D2234PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/807,499
 C--> 11 <141> CURRENT FILING DATE: 2001-04-13
 13 <150> PRIOR APPLICATION NUMBER: DE 198 47 064.9
 14 <151> PRIOR FILING DATE: 1998-10-13
 16 <160> NUMBER OF SEQ ID NOS: 22
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 907
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Rattus norvegicus
 25 <400> SEQUENCE: 1
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 27 1 5 10 15
 29 Val Gly Ala Asn Phe Pro Asn Asn Ile Gln Ile Gly Gly Leu Phe Pro
 30 20 25 30
 32 Asn Gln Gln Ser Gln Glu His Ala Ala Phe Arg Phe Ala Leu Ser Gln
 33 35 40 45
 35 Leu Thr Glu Pro Pro Lys Leu Leu Pro Gln Ile Asp Ile Val Asn Ile
 36 50 55 60
 38 Ser Asp Ser Phe Glu Met Thr Tyr Arg Phe Cys Ser Gln Phe Ser Lys
 39 65 70 75 80
 41 Gly Val Tyr Ala Ile Phe Gly Phe Tyr Glu Arg Arg Thr Val Asn Met
 42 85 90 95
 44 Leu Thr Ser Phe Cys Gly Ala Leu His Val Cys Phe Ile Thr Pro Ser
 45 100 105 110
 47 Phe Pro Val Asp Thr Ser Asn Gln Phe Val Leu Gln Leu Arg Pro Glu
 48 115 120 125
 50 Leu Gln Glu Ala Leu Ile Ser Ile Ile Asp His Tyr Lys Trp Gln Thr
 51 130 135 140
 53 Phe Val Tyr Ile Tyr Asp Ala Asp Arg Gly Leu Ser Val Leu Gln Arg
 54 145 150 155 160
 56 Val Leu Asp Thr Ala Ala Glu Lys Asn Trp Gln Val Thr Ala Val Asn
 57 165 170 175
 59 Ile Leu Thr Thr Thr Glu Glu Gly Tyr Arg Met Leu Phe Gln Asp Leu
 60 180 185 190
 62 Glu Lys Lys Lys Glu Arg Leu Val Val Val Asp Cys Glu Ser Glu Arg
 63 195 200 205
 65 Leu Asn Ala Ile Leu Gly Gln Ile Val Lys Leu Glu Lys Asn Gly Ile
 66 210 215 220
 68 Gly Tyr His Tyr Ile Leu Ala Asn Leu Gly Phe Met Asp Ile Asp Leu
 69 225 230 235 240
 71 Asn Lys Phe Lys Glu Ser Gly Ala Asn Val Thr Gly Phe Gln Leu Val
 72 245 250 255

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74 Asn Tyr Thr Asp Thr Ile Pro Ala Arg Ile Met Gln Gln Trp Arg Thr
75           260           265           270
77 Ser Asp Ser Arg Asp His Thr Arg Val Asp Trp Lys Arg Pro Lys Tyr
78           275           280           285
80 Thr Ser Ala Leu Thr Tyr Asp Gly Val Lys Val Met Ala Glu Ala Phe
81           290           295           300
83 Gln Ser Leu Arg Arg Gln Arg Ile Asp Ile Ser Arg Arg Gly Asn Ala
84 305           310           315           320
86 Gly Asp Cys Leu Ala Asn Pro Ala Val Pro Trp Gly Gln Gly Ile Asp
87           325           330           335
89 Ile Gln Arg Ala Leu Gln Gln Val Arg Phe Glu Gly Leu Thr Gly Asn
90           340           345           350
92 Val Gln Phe Asn Glu Lys Gly Arg Arg Thr Asn Tyr Thr Leu His Val
93           355           360           365
95 Ile Glu Met Lys His Asp Gly Ile Arg Lys Ile Gly Tyr Trp Asn Glu
96           370           375           380
98 Asp Asp Lys Phe Val Pro Ala Ala Thr Asp Ala Gln Ala Gly Gly Asp
99 385           390           395           400
101 Asn Ser Ser Val Gln Asn Arg Thr Tyr Ile Val Thr Thr Ile Leu Glu
102           405           410           415
104 Asp Pro Tyr Val Met Leu Lys Lys Asn Ala Asn Gln Phe Glu Gly Asn
105           420           425           430
107 Asp Arg Tyr Glu Gly Tyr Cys Val Glu Leu Ala Ala Glu Ile Ala Lys
108           435           440           445
110 His Val Gly Tyr Ser Tyr Arg Leu Glu Ile Val Ser Asp Gly Lys Tyr
111           450           455           460
113 Gly Ala Arg Asp Pro Asp Thr Lys Ala Trp Asn Gly Met Val Gly Glu
114 465           470           475           480
116 Leu Val Tyr Gly Arg Ala Asp Val Ala Val Ala Pro Leu Thr Ile Thr
117           485           490           495
119 Leu Val Arg Glu Glu Val Ile Asp Phe Ser Lys Pro Phe Met Ser Leu
120           500           505           510
122 Gly Ile Ser Ile Met Ile Lys Lys Pro Gln Lys Ser Lys Pro Gly Val
123           515           520           525
125 Phe Ser Phe Leu Asp Pro Leu Ala Tyr Glu Ile Trp Met Cys Ile Val
126           530           535           540
128 Phe Ala Tyr Ile Gly Val Ser Val Val Leu Phe Leu Val Ser Arg Phe
129 545           550           555           560
131 Ser Pro Tyr Glu Trp His Ser Glu Glu Phe Glu Glu Gly Arg Asp Gln
132           565           570           575
134 Thr Thr Ser Asp Gln Ser Asn Glu Phe Gly Ile Phe Asn Ser Leu Trp
135           580           585           590
137 Phe Ser Leu Gly Ala Phe Met Gln Gln Gly Cys Asp Ile Ser Pro Arg
138           595           600           605
140 Ser Leu Ser Gly Arg Ile Val Gly Gly Val Trp Trp Phe Phe Thr Leu
141           610           615           620
143 Ile Ile Ile Ser Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Thr Val
144 625           630           635           640
146 Glu Arg Met Val Ser Pro Ile Glu Ser Ala Glu Asp Leu Ala Lys Gln

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147          645          650          655
149 Thr Glu Ile Ala Tyr Gly Thr Leu Glu Ala Gly Ser Thr Lys Glu Phe
150          660          665          670
152 Phe Arg Arg Ser Lys Ile Ala Val Phe Glu Lys Met Trp Thr Tyr Met
153          675          680          685
155 Lys Ser Ala Glu Pro Ser Val Phe Val Arg Thr Thr Glu Glu Gly Met
156          690          695          700
158 Ile Arg Val Arg Lys Ser Lys Gly Lys Tyr Ala Tyr Leu Leu Glu Ser
159 705          710          715          720
161 Thr Met Asn Glu Tyr Ile Glu Gln Arg Lys Pro Cys Asp Thr Met Lys
162          725          730          735
164 Val Gly Gly Asn Leu Asp Ser Lys Gly Tyr Gly Ile Ala Thr Pro Lys
165          740          745          750
167 Gly Ser Ala Leu Arg Asn Pro Val Asn Leu Ala Val Leu Lys Leu Asn
168          755          760          765
170 Glu Gln Gly Leu Leu Asp Lys Leu Lys Asn Lys Trp Trp Tyr Asp Lys
171          770          775          780
173 Gly Glu Cys Gly Ser Gly Gly Gly Asp Ser Lys Asp Lys Thr Ser Ala
174 785          790          795          800
176 Leu Ser Leu Ser Asn Val Ala Gly Val Phe Tyr Ile Leu Ile Gly Gly
177          805          810          815
179 Leu Gly Leu Ala Met Leu Val Ala Leu Ile Glu Phe Cys Tyr Lys Ser
180          820          825          830
182 Arg Ser Glu Ser Lys Arg Met Lys Gly Phe Cys Leu Ile Pro Gln Gln
183          835          840          845
185 Ser Ile Asn Glu Ala Ile Arg Thr Ser Thr Leu Pro Arg Asn Ser Gly
186          850          855          860
188 Ala Gly Ala Ser Gly Gly Gly Gly Ser Gly Glu Asn Gly Arg Val Val
189 865          870          875          880
191 Ser Gln Asp Phe Pro Lys Ser Met Gln Ser Ile Pro Cys Met Ser His
192          885          890          895
194 Ser Ser Gly Met Pro Leu Gly Ala Thr Gly Leu
195          900          905
199 <210> SEQ ID NO: 2
200 <211> LENGTH: 883
201 <212> TYPE: PRT
202 <213> ORGANISM: Rattus norvegicus
204 <400> SEQUENCE: 2
205 Met Gln Lys Ile Met His Ile Ser Val Leu Leu Ser Pro Val Leu Trp
206 1          5          10          15
208 Gly Leu Ile Phe Gly Val Ser Ser Asn Ser Ile Gln Ile Gly Gly Leu
209          20          25          30
211 Phe Pro Arg Gly Ala Asp Gln Glu Tyr Ser Ala Phe Arg Val Gly Met
212          35          40          45
214 Val Gln Phe Ser Thr Ser Glu Phe Arg Leu Thr Pro His Ile Asp Asn
215          50          55          60
217 Leu Glu Val Ala Asn Ser Phe Ala Val Thr Asn Ala Phe Cys Ser Gln
218 65          70          75          80
220 Phe Ser Arg Gly Val Tyr Ala Ile Phe Gly Phe Tyr Asp Lys Lys Ser

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221		85		90		95
223	Val Asn Thr	Ile Thr Ser Phe Cys Gly Thr Leu His Val Ser Phe Ile				
224		100		105		110
226	Thr Pro Ser Phe Pro Thr Asp Gly Thr His Pro Phe Val Ile Gln Met					
227		115		120		125
229	Arg Pro Asp Leu Lys Gly Ala Leu Leu Ser Leu Ile Glu Tyr Tyr Gln					
230		130		135		140
232	Trp Asp Lys Phe Ala Tyr Leu Tyr Asp Ser Asp Arg Gly Leu Ser Thr					
233	145		150		155	160
235	Leu Gln Ala Val Leu Asp Ser Ala Ala Glu Lys Lys Trp Gln Val Thr					
236		165		170		175
238	Ala Ile Asn Val Gly Asn Ile Asn Asn Asp Lys Lys Asp Glu Thr Tyr					
239		180		185		190
241	Arg Ser Leu Phe Gln Asp Leu Glu Leu Lys Lys Glu Arg Arg Val Ile					
242		195		200		205
244	Leu Asp Cys Glu Arg Asp Lys Val Asn Asp Ile Val Asp Gln Val Ile					
245		210		215		220
247	Thr Ile Gly Lys His Val Lys Gly Tyr His Tyr Ile Ile Ala Asn Leu					
248	225		230		235	240
250	Gly Phe Thr Asp Gly Asp Leu Leu Lys Ile Gln Phe Gly Gly Ala Asn					
251		245		250		255
253	Val Ser Gly Phe Gln Ile Val Asp Tyr Asp Asp Ser Leu Val Ser Lys					
254		260		265		270
256	Phe Ile Glu Arg Trp Ser Thr Leu Glu Glu Lys Glu Tyr Pro Gly Ala					
257		275		280		285
259	His Thr Ala Thr Ile Lys Tyr Thr Ser Ala Leu Thr Tyr Asp Ala Val					
260		290		295		300
262	Gln Val Met Thr Glu Ala Phe Arg Asn Leu Arg Lys Gln Arg Ile Glu					
263	305		310		315	320
265	Ile Ser Arg Arg Gly Asn Ala Gly Asp Cys Leu Ala Asn Pro Ala Val					
266		325		330		335
268	Pro Trp Gly Gln Gly Val Glu Ile Glu Arg Ala Leu Lys Gln Val Gln					
269		340		345		350
271	Val Glu Gly Leu Ser Gly Asn Ile Lys Phe Asp Gln Asn Gly Lys Arg					
272		355		360		365
274	Ile Asn Tyr Thr Ile Asn Ile Met Glu Leu Lys Thr Asn Gly Pro Arg					
275		370		375		380
277	Lys Ile Gly Tyr Trp Ser Glu Val Asp Lys Met Val Val Thr Leu Thr					
278	385		390		395	400
280	Glu Leu Pro Ser Gly Asn Asp Thr Ser Gly Leu Glu Asn Lys Thr Val					
281		405		410		415
283	Val Val Thr Thr Ile Leu Glu Ser Pro Tyr Val Met Met Lys Lys Asn					
284		420		425		430
286	His Glu Met Leu Glu Gly Asn Glu Arg Tyr Glu Gly Tyr Cys Val Asp					
287		435		440		445
289	Leu Ala Ala Glu Ile Ala Lys His Cys Gly Phe Lys Tyr Lys Leu Thr					
290		450		455		460
292	Ile Val Gly Asp Gly Lys Tyr Gly Ala Arg Asp Ala Asp Thr Lys Ile					
293	465		470		475	480

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295 Trp Asn Gly Met Val Gly Glu Leu Val Tyr Gly Lys Ala Asp Ile Ala
296                               485                               490                               495
298 Ile Ala Pro Leu Thr Ile Thr Leu Val Arg Glu Glu Val Ile Asp Phe
299                               500                               505                               510
301 Ser Lys Pro Phe Met Ser Leu Gly Ile Ser Ile Met Ile Lys Lys Pro
302                               515                               520                               525
304 Gln Lys Ser Lys Pro Gly Val Phe Ser Phe Leu Asp Pro Leu Ala Tyr
305                               530                               535                               540
307 Glu Ile Trp Met Cys Ile Val Phe Ala Tyr Ile Gly Val Ser Val Val
308 545                               550                               555                               560
310 Leu Phe Leu Val Ser Arg Phe Ser Pro Tyr Glu Trp His Thr Glu Glu
311                               565                               570                               575
313 Phe Glu Asp Gly Arg Glu Thr Gln Ser Ser Glu Ser Thr Asn Glu Phe
314                               580                               585                               590
316 Gly Ile Phe Asn Ser Leu Trp Phe Ser Leu Gly Ala Phe Met Arg Gln
317                               595                               600                               605
319 Gly Cys Asp Ile Ser Pro Arg Ser Leu Ser Gly Arg Ile Val Gly Gly
320                               610                               615                               620
322 Val Trp Trp Phe Phe Thr Leu Ile Ile Ile Ser Ser Tyr Thr Ala Asn
323 625                               630                               635                               640
325 Leu Ala Ala Phe Leu Thr Val Glu Arg Met Val Ser Pro Ile Glu Ser
326                               645                               650                               655
328 Ala Glu Asp Leu Ser Lys Gln Thr Glu Ile Ala Tyr Gly Thr Leu Asp
329                               660                               665                               670
331 Ser Gly Ser Thr Lys Glu Phe Phe Arg Arg Ser Lys Ile Ala Val Phe
332                               675                               680                               685
334 Asp Lys Met Trp Thr Tyr Met Arg Ser Ala Glu Pro Ser Val Phe Val
335                               690                               695                               700
337 Arg Thr Thr Ala Glu Gly Val Ala Arg Val Arg Lys Ser Lys Gly Lys
338 705                               710                               715                               720
340 Tyr Ala Tyr Leu Leu Glu Ser Thr Met Asn Glu Tyr Ile Glu Gln Arg
341                               725                               730                               735
343 Lys Pro Cys Asp Thr Met Lys Val Gly Gly Asn Leu Asp Ser Lys Gly
344                               740                               745                               750
346 Tyr Gly Ile Ala Thr Pro Lys Gly Ser Ser Leu Gly Asn Ala Val Asn
347                               755                               760                               765
349 Leu Ala Val Leu Lys Leu Asn Glu Gln Gly Leu Leu Asp Lys Leu Lys
350                               770                               775                               780
352 Asn Lys Trp Trp Tyr Asp Lys Gly Glu Cys Gly Ser Gly Gly Gly Asp
353 785                               790                               795                               800
355 Ser Lys Glu Lys Thr Ser Ala Leu Ser Leu Ser Asn Val Ala Gly Val
356                               805                               810                               815
358 Phe Tyr Ile Leu Val Gly Gly Leu Gly Leu Ala Met Leu Val Ala Leu
359                               820                               825                               830
361 Ile Glu Phe Cys Tyr Lys Ser Arg Ala Glu Ala Lys Arg Met Lys Val
362                               835                               840                               845
364 Ala Lys Asn Pro Gln Asn Ile Asn Pro Ser Ser Ser Gln Asn Ser Gln
365                               850                               855                               860
367 Asn Phe Ala Thr Tyr Lys Glu Gly Tyr Asn Val Tyr Gly Ile Glu Ser

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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TIME: 13:34:34

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\05112001\I807499.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1858 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

L:1917 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:1975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13

L:2033 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:2091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15

L:2151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:2210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

L:2268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:2326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19

L:2386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20